

(FILE 'HOME' ENTERED AT 09:53:57 ON 08 FEB 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 09:54:01 ON 08 FEB
2005

L1	58 S KLUYVEROMYCES (2N) AESTUARII
L2	8 S L1 AND (CARBONYL (2N) REDUCTASE)
L3	6 DUP REM L2 (2 DUPLICATES REMOVED)

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1539	100.0	292	3	US-09-468-738A-2	Sequence 2, Appli
2	1539	100.0	292	4	US-09-940-019-2	Sequence 2, Appli
3	1539	100.0	292	4	US-09-940-037A-2	Sequence 2, Appli
4	1539	100.0	296	3	US-09-468-738A-23	Sequence 23, Appl
5	1539	100.0	296	4	US-09-940-019-23	Sequence 23, Appl
6	1539	100.0	296	4	US-09-940-037A-23	Sequence 23, Appl
7	827	53.7	290	4	US-09-248-796A-16592	Sequence 16592, A
8	621	40.4	308	4	US-09-248-796A-16593	Sequence 16593, A
9	558.5	36.3	283	3	US-09-367-012-1	Sequence 1, Appli
10	558.5	36.3	283	4	US-09-777-157A-1	Sequence 1, Appli
11	363.5	23.6	316	4	US-09-489-039A-12990	Sequence 12990, A
12	337	21.9	257	3	US-09-134-001C-3562	Sequence 3562, Ap
13	294.5	19.1	111	4	US-09-248-796A-16591	Sequence 16591, A
14	289.5	18.8	251	4	US-09-922-501-16	Sequence 16, Appl
15	289.5	18.8	306	4	US-09-710-279-382	Sequence 382, App
16	288	18.7	254	4	US-09-978-758-2	Sequence 2, Appli
17	287.5	18.7	274	3	US-09-134-001C-4431	Sequence 4431, Ap
18	283.5	18.4	253	4	US-09-543-681A-6693	Sequence 6693, Ap

6, 416, 986

6, 485, 948

RESULT 2

US-09-940-019-2

; Sequence 2, Application US/09940019

: Patent No. 6416986

; GENERAL INFORMATION:

; APPLICANT: Kimoto, No. 6416986ihiro

; APPLICANT: Yamamoto, Hiroaki

; APPLICANT: Mitsuhashi, Kazuya

; TITLE OF INVENTION: NOVEL CARBOXYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA

; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL
USING SAID

; TITLE OF INVENTION: ENZYME

; FILE REFERENCE: 06501-050001

; CURRENT APPLICATION NUMBER: US/09/940,019

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 09/468,738

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: JP 1998-363130

; PRIOR FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1

; SEQ ID NO 2

; LENGTH: 292

```
; TYPE: PRT
```

; ORGANISM: Kluyveromyces aestuarii

US-09-940-019-2

Query Match 100.0%; Score 1539; DB 4; Length 292;

Best Local Similarity 100.0%; Pred. No. 1.1e-153;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFQHFLRGGLDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60

|||||

Db 1 MTFOHFLRGGLEDKTVPOEPPKEOYPDGVNYLSLFSOKGKLTVITGGAGAIGGALCEGFA 60

RESULT 3

US-09-940-037A-2

; Sequence 2, Application US/09940037A
 ; Patent No. 6485948
 ; GENERAL INFORMATION:
 ; APPLICANT: Kimoto, No. 6485948ihiro
 ; APPLICANT: Yamamoto, Hiroaki
 ; APPLICANT: Mitsuhashi, Kazuya
 ; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID
 ENZYME, DNA
 ; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL
 USING SAID
 ; TITLE OF INVENTION: ENZYME
 ; FILE REFERENCE: 06501-050001
 ; CURRENT APPLICATION NUMBER: US/09/940,037A
 ; CURRENT FILING DATE: 2000-08-27
 ; PRIOR APPLICATION NUMBER: 09/468,738
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: JP 1998-363130
 ; PRIOR FILING DATE: 1998-12-21
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1
 ; SEQ ID NO 2
 ; LENGTH: 292
 ; TYPE: PRT
 ; ORGANISM: Kluyveromyces aestuarii
 US-09-940-037A-2

Query Match 100.0%; Score 1539; DB 4; Length 292;
 Best Local Similarity 100.0%; Pred. No. 1.1e-153;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MTFQHFLRGGLEDKTVPQEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA 60

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	1539	100.0	292	9	US-09-940-019-2	Sequence 2, Appli	
2	1539	100.0	292	9	US-09-940-037A-2	Sequence 2, Appli	
3	1539	100.0	292	12	US-09-855-309-2	Sequence 2, Appli	
4	1539	100.0	296	9	US-09-940-019-23	Sequence 23, Appl	
5	1539	100.0	296	9	US-09-940-037A-23	Sequence 23, Appl	
6	1539	100.0	296	12	US-09-855-309-23	Sequence 23, Appl	
7	852	55.4	282	14	US-10-032-585-7746	Sequence 7746, Ap	

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	558.5	36.3	283	2	JC7338	carbonyl reductase
2	510.5	33.2	255	2	T39164	sorbitol utilizati
3	451.5	29.3	261	2	T41116	short chain dehydr
4	407	26.4	261	2	T38157	short-chain dehydr
5	396	25.7	257	2	A72395	oxidoreductase, sh
6	352.5	22.9	255	2	D70635	hypothetical prote
7	335.5	21.8	271	2	AC0157	probable short cha
8	331.5	21.5	262	2	AG2809	short chain dehydr
9	331.5	21.5	262	2	B97588	oxidoreductase, sh
10	313.5	20.4	282	1	JC4041	D-arabinitol 2-deh
11	303.5	19.7	281	2	F69400	2-deoxy-D-gluconat
12	301	19.6	298	2	AI3058	gluconate 5-dehydr

Database : UniProt_02:*.
 1: uniprot_sprot:*.
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1534	99.7	292	2	Q75WS0	Q75ws0 kluyveromyc	
2	1534	99.7	292	2	BAD01116	Bad01116 kluyverom	
3	1289	83.8	292	2	Q6CM75	Q6cm75 kluyveromyc	
4	864.5	56.2	286	2	Q6BXW6	Q6bxw6 debaryomyce	
5	644	41.8	278	2	Q6CEE9	Q6cee9 yarrowia li	
6	637	41.4	279	2	Q6BQ25	Q6bq25 debaryomyce	
7	624	40.5	280	1	SOU2_CANAL	P87218 candida alb	
8	622.5	40.4	281	1	SOU1_CANAL	P87219 candida alb	
9	619	40.2	291	2	Q6BN16	Q6bn16 debaryomyce	
10	607	39.4	280	2	Q6CM06	Q6cm06 kluyveromyc	
11	605.5	39.3	285	2	Q6BQ28	Q6bq28 debaryomyce	

RESULT 1

Q75WS0

ID Q75WS0 PRELIMINARY; PRT; 292 AA.
AC Q75WS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Carbonyl reductase.
GN Name=kacr1;
OS Kluyveromyces aestuarii.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=33165;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto H., Mitsuhashi K., Kimoto N., Matsuyama A., Esaki N.,
RA Kobayashi Y.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
DR EMBL; AB120765; BAD01116.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDHRDH.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 292 AA; 31685 MW; 0165CCCB430EF7DA CRC64;

Query Match 99.7%; Score 1534; DB 2; Length 292;
Best Local Similarity 99.7%; Pred. No. 2.7e-113;
Matches 291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTFQHFLRGGLEDKTVPEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA	60
Db	1	MTFQHFLRGGLEDKTVPEPPKEQYPDGVNYLSLFSQKGKLTVITGGAGAIGGALCEGFA	60
Qy	61	SCGSDVVILDYKYSPELSSVLESRYGVRKSYQVDITSSQKLVVAKILEDFFPDRDINT	120
Db	61	SCGSDVVILDYKYSPELSSVLESRYGVRKSYQVDITSSQKLVVAKILEDFFPDRDINT	120
Qy	121	FVANAGIAWTNGSILNENATPDVWKRMDVNVQGTYHCAKYVAEVFKQQGHGNLILTASM	180
Db	121	FVANAGIAWTNGSILNENATPDVWKRMDVNVQGTYHCAKYVAEVFKQQGHGNLILTASM	180
Qy	181	SSYISNVPNYQTCYNASKAAVRHMAKGFVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV	240
Db	181	SSYISNVPNYQTCYNASKAAVRHMAKGFVEFAHLTNPAGKIRCNSVSPGYTDTALSAFV	240
Qy	241	PVEQRAQWWGLTPMGREALPQELVGAYLYLASDAASFTNGCDIQVDGGYTCV	292
Db	241	PVEQRAQWWGLTPMGREALPQEXVGAYLYLASDAASFTNGCDIQVDGGYTCV	292